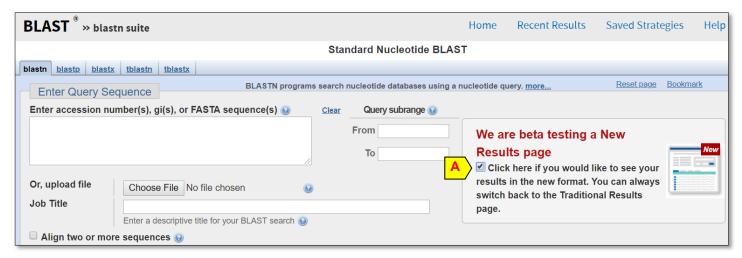
Scope

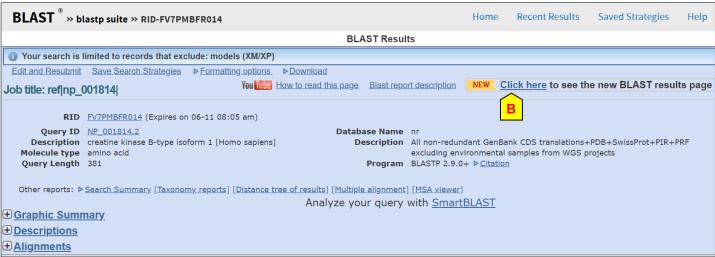
NCBI recently released an enhanced BLAST result display early 2019 (https://go.usa.gov/xyq5Y). This display will become the new default at the end of August, 2019, to coincide with the start of the new school year. The current default will be available as an alternative format until its retirement at the end of 2019. This new display:

- reduces the need of scrolling by placing each section of the BLAST results into their own tab
- makes result filtering easier by bringing the control to the front
- allows convenient download by arranging the option close to the result
- integrates the taxonomy report by placing its access as an new tab

Access to BLAST and the New BLAST Result Page

Access to NCBI BLAST web services through its homepage (blast.ncbi.nlm.nih.gov) remains the same as before. The change is in the layout of the display of the results after a search is completed. Before this display becomes default, there are two ways to access the new display: set it as default by clicking the checkbox in the advertisement, such as the one in the nucleotide search form (A), or using the link (B) at the top of the result page.



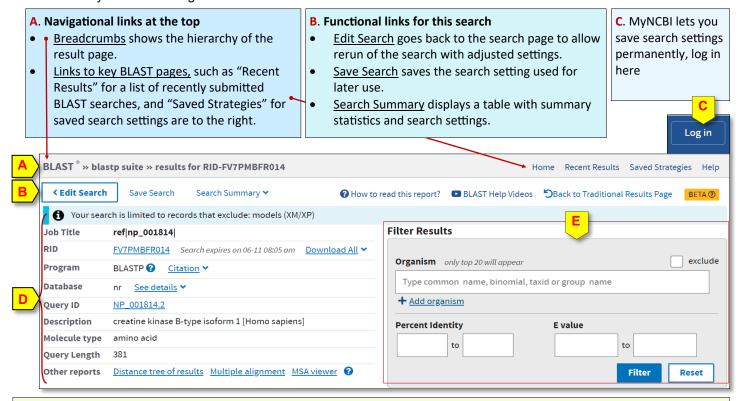


The general structure of the BLAST result page essentially stays the same, which contains the Summary, Graphical Overview, Descriptions table, and Alignments sections. The enhancements are in the following areas: 1) the Summary section is restructured to make the information more readable, 2) key post-search result filters are brought to the front, making them readily accessible, 3) remaining sections are reported in their own tabs below the Summary, 4) the Taxonomy report is integrated into this tab-formatted display, and 5) filters applied acts uniformly on Descriptions, Alignments, Taxonomy, as well as their download.

The New BLAST Results Page

The Summary Section

The Summary section (shown below) is at the top of a result page. This section display is always on and is independent of which of the remaining sections is selected for display in the tabs below so you can know what you searched with and the database you searched against.



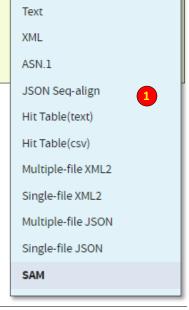
D. Summary provides information on different aspects of the search

- <u>Highlighted message box</u> displays reminder, warning, or errors if relevant.
- Job Title shows the first guery's sequence id by default, for more better search identification customize it before submission.
- <u>RID</u> shows the assigned unique identifier to this search for sharing and problem reporting; <u>Download All</u> shows a list of options to save the complete search result in desired format (1), such as new XML (XML2), JSON, and CSV.
- Results for (not present for single query search) allows selection of the input query for which to show the search results.
- <u>Program</u> lists the search conducted, blastp in this case; <u>Citation</u> provides the reference to cite in your publication.
- <u>Database</u> names the target database searched; <u>See details</u> provides a text description of the content.
- Query ID is the query's sequence id for which the result is shown. If accession is used, it is linked to the record in NCBI database.
- <u>Description</u> is the title of the query sequence from its FASTA defline.
- Molecule type shows the type of the sequence.
- Query length is the length of the current query.
- Other reports lists links to other report formats not integrated to the new tab-based display. Multiple alignment links to COBALT search, which is not available for nucleotide BLAST.

E. Filter Results

- Organism allows input of organism name (select from auto-suggested list) to filter the returned hits. Check the <u>exclude checkbox</u> to exclude selected organism from display. Need more organisms? click <u>Add organism</u> to add additional field.
- <u>Percent Identity</u> allows filtering of hits by degree of identity, such as between 94.74 and 94.76 percent.
- E Value filters result by hits' significance in Expect value, such as between 0.0001 and 5e-120 (5x10⁻¹²⁰).

Enter the desired values, then click <u>Filter</u> to update the result display. The Filter works through post-processing and does not change the returned search. Click <u>Reset</u> to see the initial set of results.



The Descriptions Section

The Descriptions tab (shown below) contains a summary table of hits found by BLAST. It is the default tab shown.

A. Three sets of pull-down menus at the top

- <u>Download</u> provides a set of options to download the selected hits (as compared to Download All in the Summary section)
- Manage Columns lists all available columns of the table so you can check or uncheck for a customized table display.
- <u>Show</u> allows you to select how many hits are shown in the table.

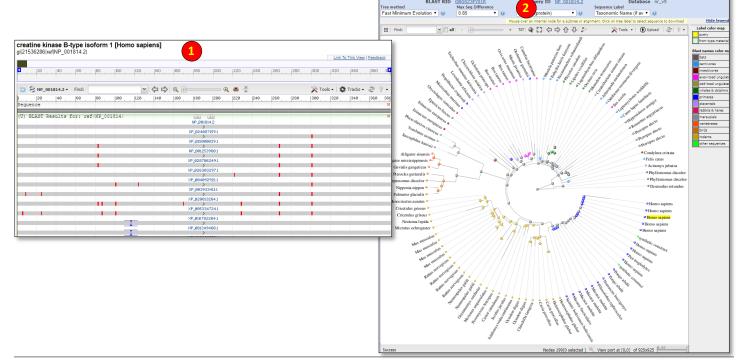
B. Functional links for this search

- <u>Select All</u> toggle on and off checkboxes for all the hits. For custom selection, click on individual checkboxes to toggle selection of specific entries.
- GenPept retrieves the full protein records for selected entries in the Protein database.
- <u>Graphics</u> links to a graphical sequence viewer-based presentation of matches anchored by the query (1).
- Distance tree of results present the matches in a distance tree format (2)
- For phylogenetic analysis, use the <u>Multiple alignment</u> link instead (protein only).



C. Table header and rows

- Default sorting is by <u>E value</u> column (in bold). Click on another header to sort by that column (not applicable to Description and Accession columns).
- Titles in the <u>Description</u> column link to the cognate alignment in the Alignments section. Click a title to jump to that location in the Alignments section to examine the actual alignment.
- Entries in the <u>Accession</u> column link to the sequence record in the Protein database or Nucleotide (for blastn or tblastn searches).



The New BLAST Results Page Page 4

The Alignments Section

The Alignments section (below) contains the detailed pairwise alignments between query and database sequences.

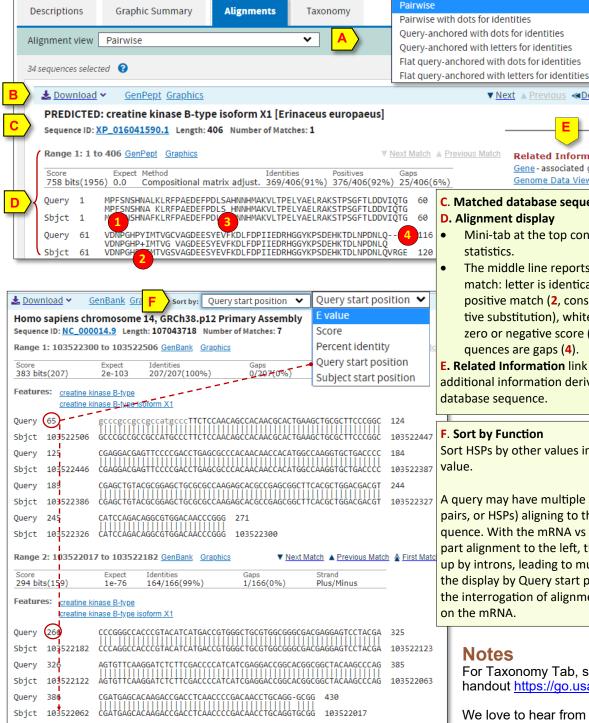
A. Alignment view

It makes alternative displays of the alignment results readily accessible through a simple pull-down menu.

B. Separator for matched database sequences

- Download lists formats available to get this matched database sequence.
- GenePept retrieves the record from the NCBI Protein database.
- Graphics links to a graphical sequence viewer-based display of the alignment between this database sequence and the query, anchored by that database sequence.
- Navigational links at the right help move between different alignments and between Alignments and Descriptions sections.

Pairwise



C. Matched database sequence

D. Alignment display

Mini-tab at the top contains the alignment statistics.

▼ Next ▲ Previous ≪ Descriptions

Related Information Gene - associated gene details

Genome Data Viewer - aligned

v

- The middle line reports the quality of the match: letter is identical match (1), + sign is positive match (2, considering it as conservative substitution), white space is match with zero or negative score (3). Dashes in the sequences are gaps (4).
- E. Related Information link to other resources with additional information derived from the matched database sequence.

F. Sort by Function

Sort HSPs by other values instead of the default E value.

A query may have multiple segments (high scoring pairs, or HSPs) aligning to the same database sequence. With the mRNA vs its genomic counterpart alignment to the left, the alignment is broken up by introns, leading to multiple HSPs. Re-sorting the display by Query start position can facilitate the interrogation of alignment by the natural order on the mRNA.

Notes

For Taxonomy Tab, see this existing handout https://go.usa.gov/xyqaY

We love to hear from our users. Please send your comments and feedback to: blast-help@ncbi.nlm.nih.gov